

SEQUENCE LISTING

<110> Whitehouse, Martha Jo

<120> Methods and Compositions for the
Treatment of Peripheral Artery Disease

<130> PP16090.004

<150> 60/213,504

<151> 2000-06-22

<150> 60/264,572

<151> 2000-01-26

<150> 60/276,549

<151> 2001-03-16

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 441

<212> DNA

<213> Bos taurus

<220>

<221> CDS

<222> (1)...(441)

<400> 1

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Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His	
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ttc aaa gat cca aaa cga cta tat tgt aaa aac ggg ggg ttc ttc cta	96
Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu	
20 25 30	

cga atc cac cca gat ggg cga gta gat ggg gta cga gaa aaa tcc gat	144
Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp	
35 40 45	

cca cac atc aaa cta caa cta caa gcc gaa gaa cga ggg gta gta tcc	192
Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser	
50 55 60	

atc aaa ggg gta tgt gcc aac cga tat cta gcc atg aaa gaa gat ggg	240
Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly	
65 70 75 80	

cga cta cta gcc tcc aaa tgt gta acc gat gaa tgt ttc ttc ttc gaa	288
Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu	
85 90 95	

cga cta gaa tcc aac aac tat aac acc tat cga tcc cga aaa tat tcc	336
Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser	
100 105 110	

tcc tgg tat gta gcc cta aaa cga acc ggg caa tat aaa cta ggg cca 384
 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
 115 120 125

aaa acc ggg cca ggg caa aaa gcc atc cta ttc cta cca atg tcc gcc 432
 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
 130 135 140

aaa tcc taa 441
 Lys Ser *
 145

<210> 2
 <211> 146
 <212> PRT
 <213> Bos taurus

<400> 2
 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
 1 5 10 15
 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
 20 25 30
 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
 35 40 45
 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
 50 55 60
 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
 65 70 75 80
 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
 85 90 95
 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Ser
 100 105 110
 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Pro
 115 120 125
 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
 130 135 140
 Lys Ser
 145

<210> 3
 <211> 441
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(441)

<400> 3
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 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
 1 5 10 15

ttc aag gac ccc aag cgg ctg tac tgc aaa aac ggg ggc ttc ttc ctg 96
 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
 20 25 30

cgc atc cac ccc gac ggc cga gtt gac ggg gtc cgg gag aag agc gac	144
Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp	
35 40 45	
cct cac atc aag cta caa ctt caa gca gaa gag aga gga gtt gtg tct	192
Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser	
50 55 60	
atc aaa gga gtg tgt gct aac cgt tac ctg gct atg aag gaa gat gga	240
Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly	
65 70 75 80	
aga tta ctg gct tct aaa tgt gtt acg gat gag tgt ttc ttt ttt gaa	288
Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu	
85 90 95	
cga ttg gaa tct aat aac tac aat act tac cgg tca agg aaa tac acc	336
Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr	
100 105 110	
agt tgg tat gtg gca ctg aaa cga act ggg cag tat aaa ctt gga tcc	384
Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser	
115 120 125	
aaa aca gga cct ggg cag aaa gct ata ctt ttt ctt cca atg tct gct	432
Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala	
130 135 140	
aag agc tga	441
Lys Ser *	
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<210> 4
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 4
 Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His
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 Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu
 20 25 30
 Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp
 35 40 45
 Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser
 50 55 60
 Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly
 65 70 75 80
 Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu
 85 90 95
 Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr
 100 105 110
 Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser
 115 120 125
 Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala
 130 135 140
 Lys Ser
 145

<210> 5
 <211> 468
 <212> DNA
 <213> Bos taurus

<220>
 <221> CDS
 <222> (1)...(468)

<400> 5
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 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
 1 5 10 15

ggg tcc ggg gcc ttc cca cca ggg cac ttc aaa gat cca aaa cga cta 96
 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
 20 25 30

tat tgt aaa aac ggg ggg ttc ttc cta cga atc cac cca gat ggg cga 144
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45

gta gat ggg gta cga gaa aaa tcc gat cca cac atc aaa cta caa cta 192
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60

caa gcc gaa gaa cga ggg gta gta tcc atc aaa ggg gta tgt gcc aac 240
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80

cga tat cta gcc atg aaa gaa gat ggg cga cta cta gcc tcc aaa tgt 288
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95

gta acc gat gaa tgt ttc ttc ttc gaa cga cta gaa tcc aac aac tat 336
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110

aac acc tat cga tcc cga aaa tat tcc tcc tgg tat gta gcc cta aaa 384
 Asn Thr Tyr Arg Ser Arg Lys Tyr Ser Ser Trp Tyr Val Ala Leu Lys
 115 120 125

cga acc ggg caa tat aaa cta ggg cca aaa acc ggg cca ggg caa aaa 432
 Arg Thr Gly Gln Tyr Lys Leu Gly Pro Lys Thr Gly Pro Gly Gln Lys
 130 135 140

gcc atc cta ttc cta cca atg tcc gcc aaa tcc taa 468
 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser *
 145 150 155

<210> 6
 <211> 155
 <212> PRT
 <213> Bos taurus

<400> 6
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 1 5 10 15
 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
 20 25 30

Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 Asn Thr Tyr Arg Ser Arg Lys Tyr Ser Ser Trp Tyr Val Ala Leu Lys
 115 120 125
 Arg Thr Gly Gln Tyr Lys Leu Gly Pro Lys Thr Gly Pro Gly Gln Lys
 130 135 140
 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
 145 150 155

<210> 7
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(468)

<400> 7
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 ggc agc ggc gcc ttc ccg ccc ggc cac ttc aag gac ccc aag cgg ctg 96
 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
 20 25 30
 tac tgc aaa aac ggg ggc ttc ttc ctg cgc atc cac ccc gac ggc cga 144
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 gtt gac ggg gtc cgg gag aag agc gac cct cac atc aag cta caa ctt 192
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 caa gca gaa gag aga gga gtt gtg tct atc aaa gga gtg tgt gct aac 240
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt 288
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 336
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ctg aaa 384
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
 115 120 125
 cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa 432

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
 130 135 140

gct ata ctt ttt ctt cca atg tct gct aag agc tga ttttaa
 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser *
 145 150 155

474

<210> 8
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 8
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 20 25 30
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
 115 120 125
 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
 130 135 140
 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
 145 150 155

<210> 9
 <211> 9
 <212> PRT
 <213> Bos taurus

<400> 9
 Met Ala Ala Gly Ser Ile Thr Thr Leu
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